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A

OsMAPK5a -----MDGAPVAE FR PTMTHGGRYLLYDI FGNKFEVFN
 OsMAPK5b -----MDGAPVAE FR PTMTHGGRYLLYDI FGNKFEVFN
 TaWCK-1 -----MDGAPVAE FR PTMTHGGRYLLYNI FGNQFEITA
 NtWIPK MADANMGAGGQGFDPF SVLTHGGQYVQFDI FGNFEITTT
 Consensus MDGAPVAE FR PTMTHGGR LLY IFGN FE T

I II
 OsMAPK5a KYOPPIMPPIGRGAYGIVCSVMNFETREMVAKKIANAFNN
 OsMAPK5b KYOPPIMPPIGRGAYGIVCSVMNFETREMVAKKIAN-----
 TaWCK-1 KYOPPIMPPIGRGAYGIVCSVMNFETREMVASKKIANAFNN
 NtWIPK KYRPPIMPPIGRGAYGIVCSVLNTELNMVAVKKIANAFDI
 Consensus KYOPPIMPPIGRGAYGIVCSVMNFETREMVAKKIANAF N

III IV
 OsMAPK5a DMDAKRTLREIKLLRHLHDHENIIGIRDVI PPPIPOAFNDV
 OsMAPK5b -----
 TaWCK-1 NMDAKRTLREIKLLRHLHDHENIVGLRDVI PPPIPOAFNDV
 NtWIPK YMDAKRTLREIKLLRHLHDHENIVGLRDVI PPPIPOAFNDV
 Consensus MDAKRTLREIKLLRHLHDHENIIGIRDVI PP IP FNDV

V
 OsMAPK5a YIATELMDTDLHHIIRSNOELSEEHCQYFLYQILRGLKYI
 OsMAPK5b -----
 TaWCK-1 YIATELMDTDLHHIIRSNOELSEEHCQYFLYQILRGLKYI
 NtWIPK YIATELMDTDLHDIIRSNOELSEHCQYFMYQILRGLKYI
 Consensus YIATELMDTDLHHIIRSNOELSEEHCQYFLYQILRGLKYI

VI VII
 OsMAPK5a HSA NVIHRDLKPSNLLLNANCDLKICDFGLARPSSSESDMM
 OsMAPK5b -----CDLKICDFGLARPSSSESDMM
 TaWCK-1 HSA NVIHRDLKPSNLLLNANCDLKICDFGLARPSSSESDMM
 NtWIPK HSA NVIHRDLKPSNLLLNANCDLKICDFGLARPNIENEM
 Consensus HSA NVIHRDLKPSNLLLNANCDLKICDFGLARPSSSESDMM

* * VIII IX
 OsMAPK5a TEYVVTRWYRAPELLNSTDYSAIDVWSVGCIEMELINR
 OsMAPK5b TEYVVTRWYRAPELLNSTDYSAIDVWSVGCIEMELINR
 TaWCK-1 TEYVVTRWYRAPELLNSTDYSAIDVWSVGCIEMELINR
 NtWIPK TEYVVTRWYRAPELLNSTDYTAIDVWSVGCIEMELINR
 Consensus TEYVVTRWYRAPELLNSTDYSAIDVWSVGCIEMELINR

X
 OsMAPK5a OPLFPGRDHMHQRLITEVIGTPTDDELGFIRNEDARKYM
 OsMAPK5b OPLFPGRDHMHQRLITEVIGTPTDDELGFIRNEDARKYM
 TaWCK-1 APLFPGRDHMHQRLITEVIGTPTDDELGFIRNEDARKYM
 NtWIPK KPLFGGKDHVHQRLLTELLGTPTDDELGFIRNEDARKYM
 Consensus PLFPGRDHMHQRLITEVIGTPTDD LGFIRNEDARKYM

XI
 OsMAPK5a RHLPOYPRRTFASMFPRVQPAALDLIERMLTFNPLQRTTV
 OsMAPK5b RHLPOYPRRTFASMFPRVQPAALDLIERMLTFNPLQRTTV
 TaWCK-1 RHLPOYPRRTFASMFPRVQPAALDLIERMLTFNPLQRTTV
 NtWIPK ROLPOHPRQOLAEVFPVHNPALDLVDKMLTFDPTTRITV
 Consensus RHLPO PRRTFAS FP VQPAALDLIERMLTFNPLQRTTV

OsMAPK5a EEALDHPYLERLHDIADEPTCLEPFSDFEOKALNE DOMK
 OsMAPK5b EEALDHPYLERLHDIADEPTCLEPFSDFEOKALNE DOMK
 TaWCK-1 EEALDHPYLERLHDIADEPTCLEPFSDFEOKALNE DOMK
 NtWIPK EEALDHPYLAKLHDAGDEPTCPVPSDFEOKGIGEEFOIK
 Consensus EEALDHPYLERLHDIADEPTCLEPFSDFEOK L EDOMK

OsMAPK5a OLIENEAEIEMNPNI RY
 OsMAPK5b OLIENEAEIEMNPNI RY
 TaWCK-1 OLIENEAEIEMNPNI RY
 NtWIPK DMIYQEALSINPEYA-
 Consensus OLIENEAEIEMNPNI RY

B

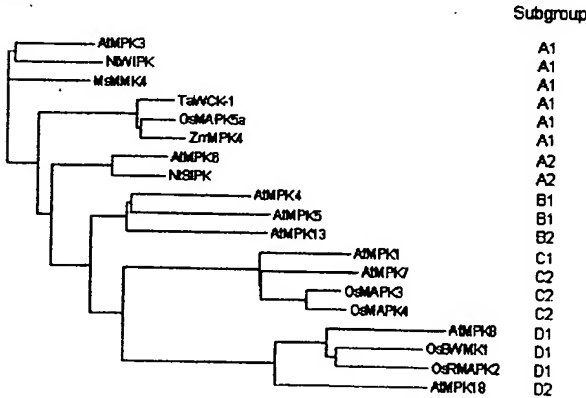


FIGURE 1

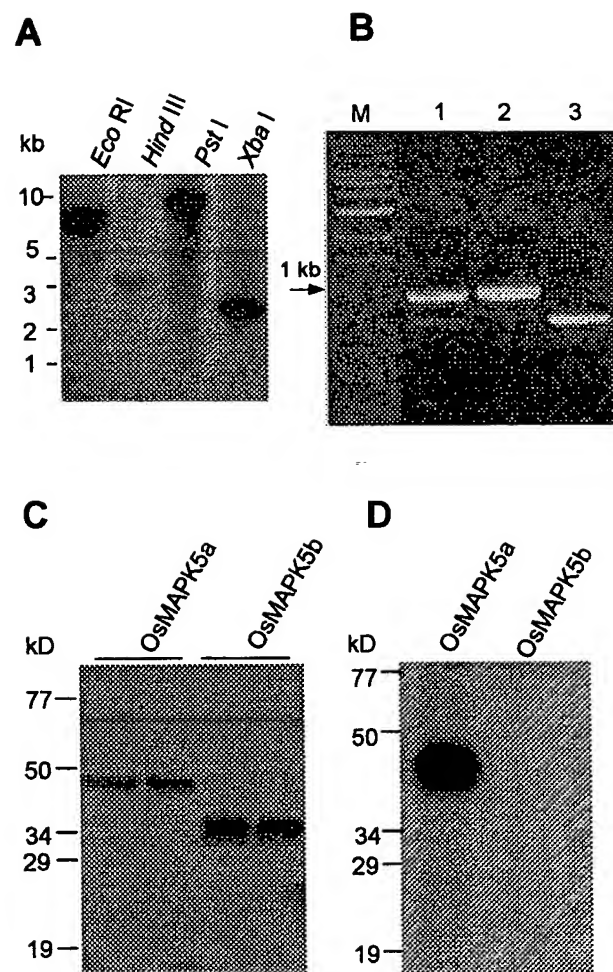


FIGURE 2

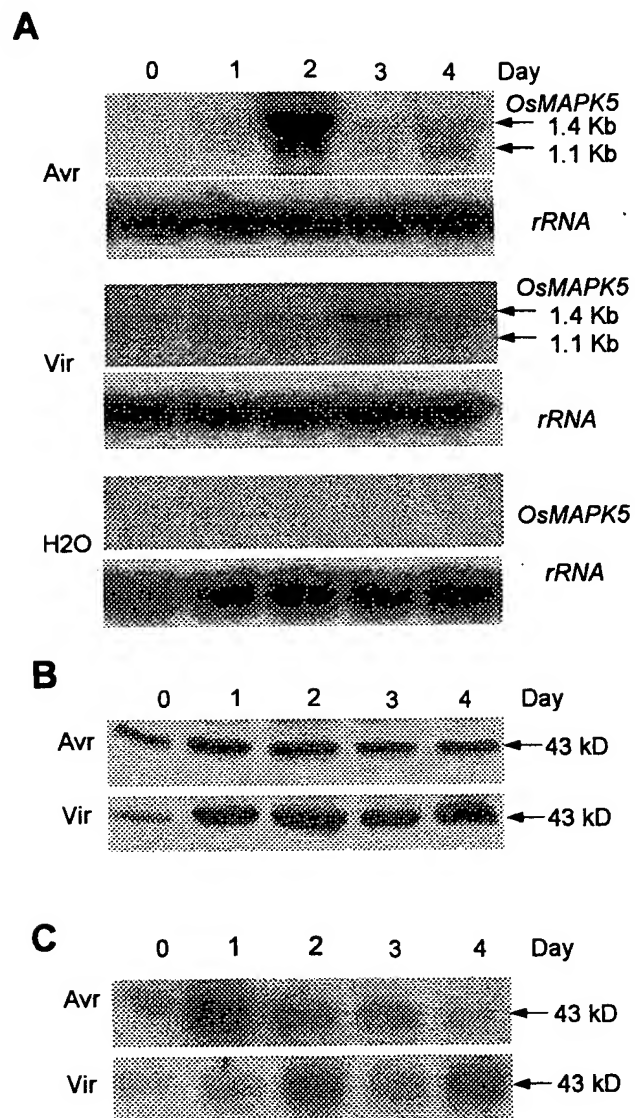


FIGURE 3

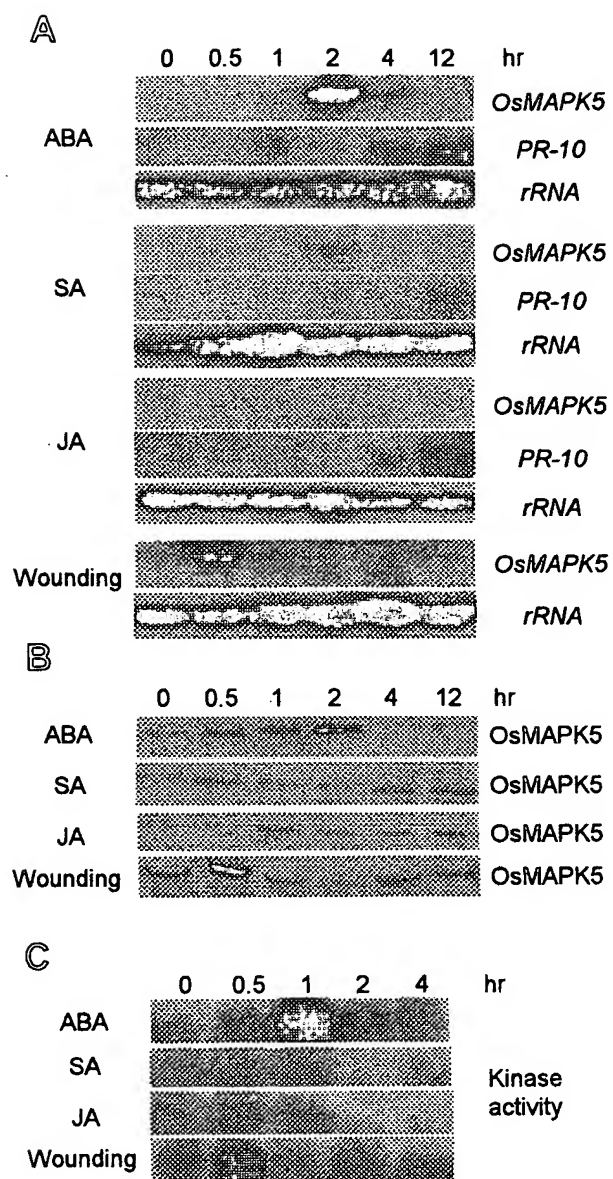
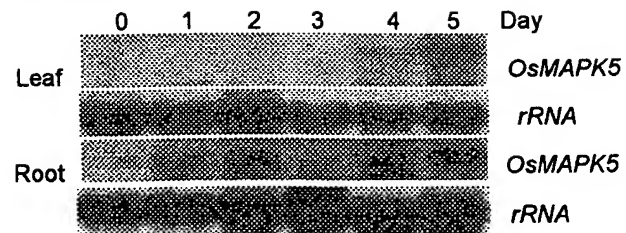
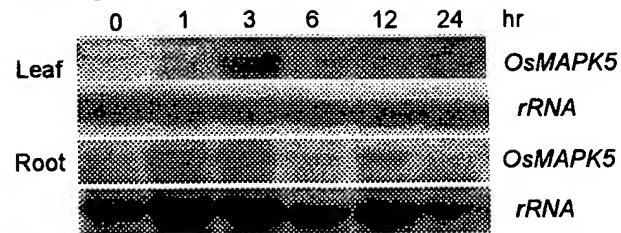
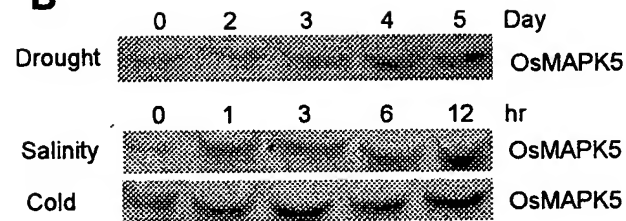
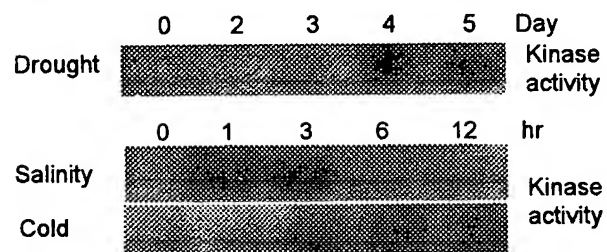


FIGURE 4

A**Drought****Salinity****Cold****B****C****FIGURE 5**

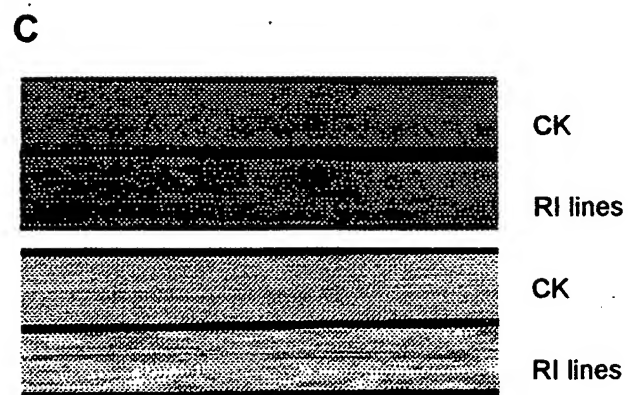
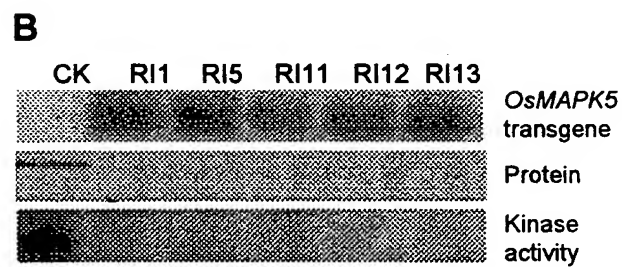
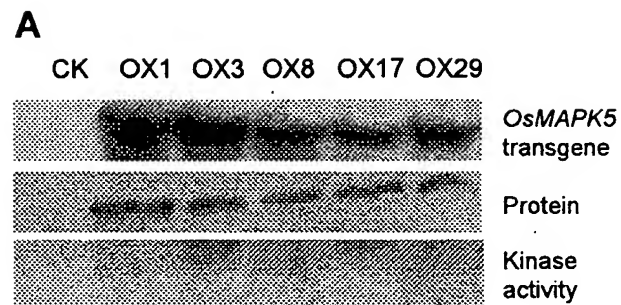
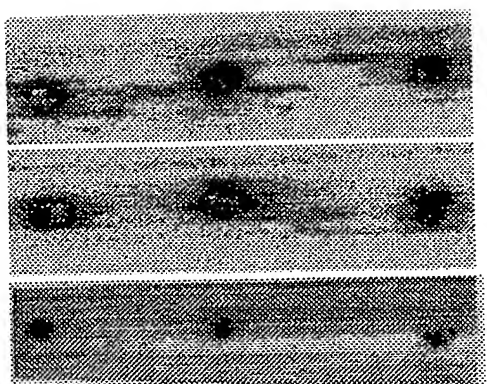
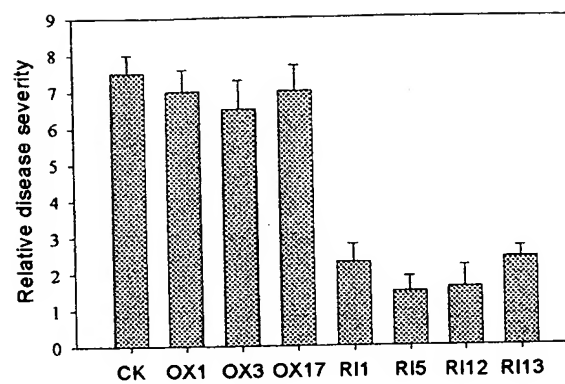
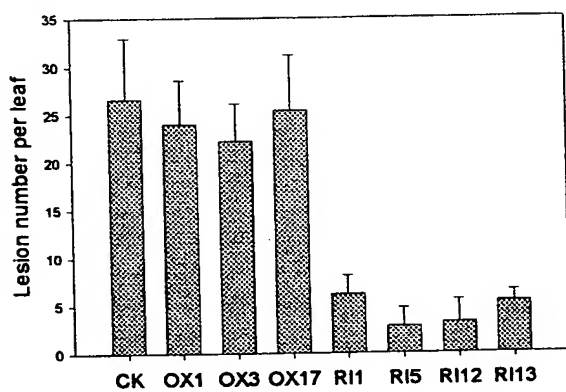
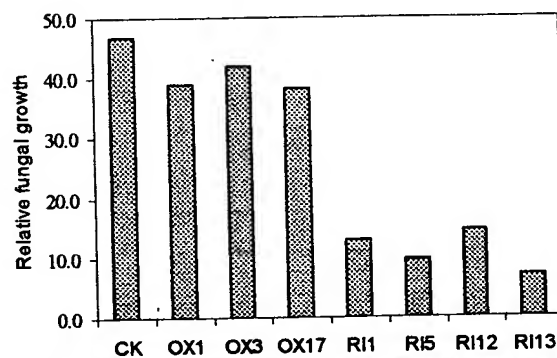
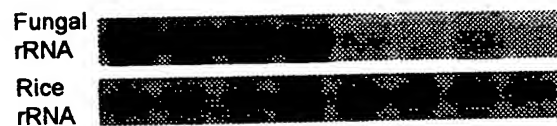
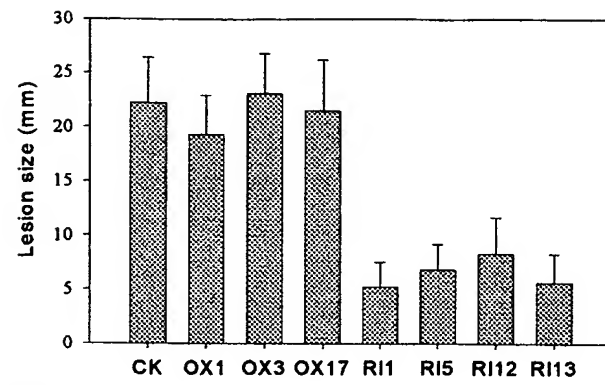
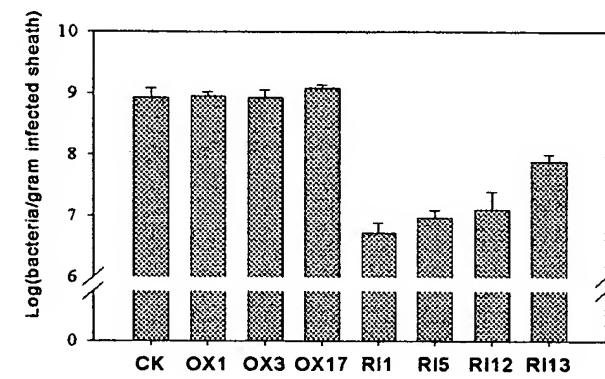


FIGURE 6

A**B****C****D****E****FIGURE 7**

A**B****C****FIGURE 8**

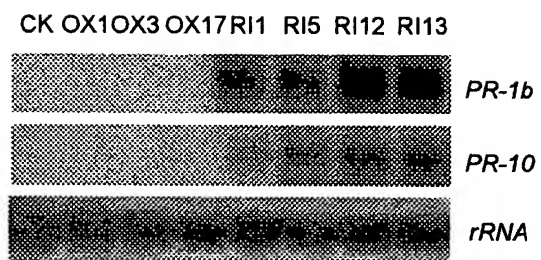
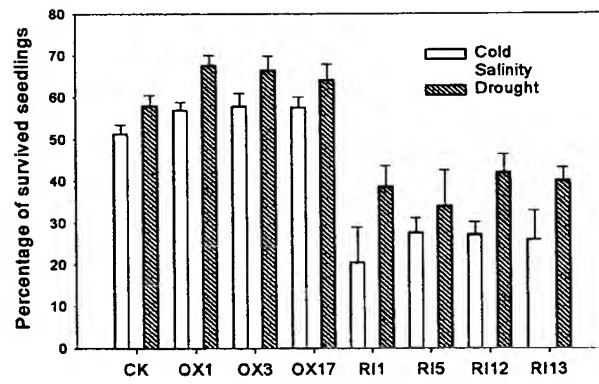
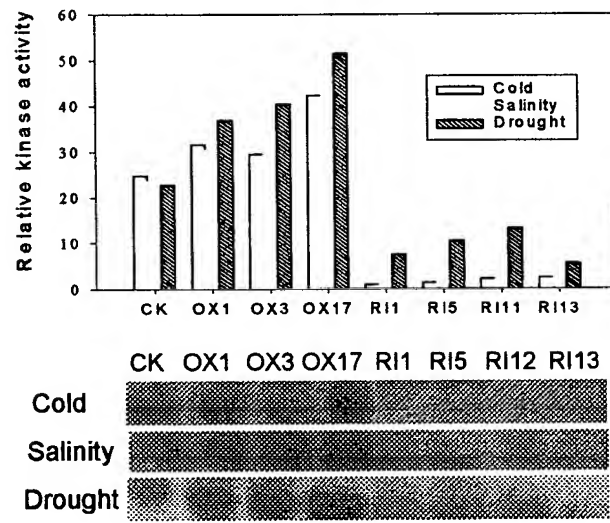


FIGURE 9

A**B****FIGURE 10**

OsMAPK5a
SEQ. ID. NO: 1

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1      agagagtcag ataaggtcgt taattagggtt ggtcaattcg gctgcttgcg gcgagagaag
61     aggaggaggg attagggatg gacggggcgc cggtggcgga gttcaggccg acgatgacgc
121    acggcggccg gtacctgctc tacgacatct tcgggaacaa gttcgagggtg acgaacaagt
181    accagccgcc catcatgccc attggccgcg gcgcctacgg gatcgtctgc tccgtgatga
241    actttgagac gagggagatg gtggcgataa agaagatcgc caacgcgttc aacaacgaca
301    tggacgccaa gcgcacgctc cgggagatca agctcctcag gcacctcgac cacgagaaca
361    tcataggcat cagggatgtg atccccgccg cgatccctca ggcgttcaac gacgtctaca
421    tcgccacgga gctcatggac accgacctcc atcacatcat ccgctccaac caagaactgt
481    cagaagagca ctgccagtat ttcctgtacc agatcctgcg ggggctcaag tacatccact
541    cggcgaacgt gatccaccgc gacctgaagc cgagcaacct gctgctgaac gccaactgcg
601    acctcaagat ctgcgacttc gggctggcgc ggccgtcgtc ggagagcgac atgatgacgg
661    agtacgtggg cacccggtgg taccgcgcgc cggagctgct gctcaactcc accgactact
721    ccgccgccat cgacgtctgg tccgtcggct gcatcttcat ggagctcatc aaccgccagc
781    cgctcttccc cggcagggac cacatgcacc agatgcgcct catcaccgag gtgatcggga
841    cgccgacgga cgacgagctg gggttcatac ggaacgagga cgcgaggaag tacatgaggc
901    acctgccgca gtaccgcgc cggacgttcg cgagcatgtt cccgcgggtg cagcccgcgc
961    cgctcgacct catcgagagg atgctcacct tcaaccgcgt gcagagaatc acagttgagg
1021   aggcgctcga tcatccttac ctagagagat tgcacgacat cgccgatgag cccatctgcc
1081   tggagccctt ctccttcgac ttcgagcaga aggctctaaa cgaggaccaa atgaagcagc
1141   tgatcttcaa cgaagcgatc gagatgaacc caaacatccg gtactagatt gaatcaccat
1201   ggaaatgaga tcccgtctat acctgctttg tacatatgat caagattgag agccgggtag
1261   actgaacatt gcatttgttt gtttgttgat gttcgaaacc cacattctct gcaagttgtg
1321   gctgctttgt atgatatatg gtactatggt cgaataaaaag ggtttggaac tttggattaa
1381   aaaaaaaaaa aaaaaa

```

FIGURE 11

OsMAPK5a
SEQ. ID. NO: 2

MDGAPVAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGR
GAYGIVCSVMNFETREMVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVI
PPPIPQAFNDVYIATELMDTDLHHIIRSNQELSEHCQYFLYQILRGLKYIHSANVIH
RDLKPSNLLLNNANCDLKICDFGLARPSSSESDMMTEYVVTRWYRAPELLNSTDYSAAI
DVWSVGCIFMELINRQPLFPGRDHMHQMRLITEVIGTPTDDELGFIRNEDARKYMRHL
PQYPRRTFASMFPRVQPAALDLIERMLTFNPLQRITVEEALDHPYLERLHDIADepIC
LEPFSFDFEQKALNEDQMKQLIFNEAIEMNPNIry

FIGURE 12

OsMAPK5b
SEQ. ID. NO: 3

```

1      agagagtcag ataaggctcgt taattagggtt ggtcaattcg gctgcttgcg gcgagagaag
61     aggaggaggg attagggatg gacggggcgc cggtggcgga gttcaggccg acgatgacgc
121    acggcgggccg gtacctgctc tacgacatct tcgggaacaa gttcgagggtg acgaacaagt
181    accagccgcc catcatgccc attggccgcg gcgcctacgg gatcgtctgc tccgtgatga
241    actttgagac gagggagatg gtggcgataa agaagatcgc caactgcgac ctcaagatct
301    gcgacttcgg gctggcgcgg ccgctcgtcg agagcgacat gatgacggag tacgtggtca
361    cccggtggta ccgcgcgcgg gagctgctgc tcaactccac cgactactcc gccgccatcg
421    acgtctggtc cgtcggctgc atcttcattg agctcatcaa ccgccagccg ctcttccccc
481    gcagggacca catgcaccag atgcgcctca tcaccgaggt gatcgggacg ccgacggacg
541    acgagctggg gttcatacgg aacgaggacg cgaggaagta catgaggcac ctgccgcagt
601    acccgcgccg gacgttcgcg agcatgttcc cgcgggtgca gcccgccgcg ctcgacctca
661    tcgagaggat gctcaccttc aacccgctgc agagaatcac agttgaggag gcgctcgatc
721    atccttacct agagagattg cacgacatcg ccgatgagcc catctgcctg gagcccttct
781    ccttcgactt cgagcagaag gctctaaacg aggaccaa at gaagcagctg atcttcaacg
841    aagcgatcga gatgaaccca aacatccggt actagattga atcaccatgg aaatgagatc
901    ccgtctatac ctgctttgta catatgatca agattgagag ccgggtagac tgaacattgc
961    atttgtttgt ttgttgatgt tcgaaaccca cattctctgc aagttgtggc tgctttgtat
1021   gatatatggt actatgttcg aataaaaggg tttggaactt tggattaaaa aaaaaaaaaa
1081   aaaa

```

FIGURE 13

OsMAPK5b

SEQ. ID. NO: 4

MMDGAPVAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGR
GAYGIVCSVMNFETREMVAIKKIANCDLKICDFGLARPSSSESDMMTEYVVTRWYRAPE
LLNSTDYSAAIDVWSVGCI FMELINRQPLFPGRDHMHQMRLITEVIGTPTDDELGFI
RNEDARKYMRHLPQYPRRTFASMFPVRVQPAALDLIERMLTFNPLQRITVEEALDHPYL
ERLHDIADepICLEPFsFDfEQKALNEDQMKQLIFNEAIEMNPNIrY

FIGURE 14